

SEQUENCE LISTING

<110> Brettman, Lee R.
 Fox, Judith A.
 Allison, David Edward

<120> Method of Administering an Antibody

<130> 1855.2007-001

<140> US 09/748,960

<141> 2000-12-27

<150> US 09/550,082

<151> 2000-04-14

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 396

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(396)

<400> 1

atg aag ttg cct gtt agg ctg ttg gtg ctt ctg ttg ttc tgg att cct	48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro	
1 5 10 15	
ggt tcc gga ggt gat gtt gtg gtg act caa act cca ctc tcc ctg cct	96
Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro	
20 25 30	
gtc agc ttt gga gat caa gtt tct atc tct tgc agg tct agt cag agt	144
Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser	
35 40 45	
ctt gca aag agt tat ggg aac acc tat ttg tct tgg tac ctg cac aag	192
Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys	
50 55 60	
cct ggc cag tct cca cag ctc ctc atc tat ggg att tcc aac aga ttt	240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe	
65 70 75 80	
tct ggg gtg cca gac agg ttc agt ggc agt ggt tca ggg aca gat ttc	288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
85 90 95	
aca ctc aag atc agc aca ata aag cct gag gac ttg gga atg tat tac	336
Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr	
100 105 110	

tgc tta caa ggt aCa cat cag ccg tac acg ttc gga ggg ggg acc aag 384
Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

ctg gaa ata aaa 396
Leu Glu Ile Lys
130

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<210> 2
<211> 132
<212> PRT
<213> Mus musculus
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<220>
<221> SIGNAL
<222> (1)...(20)
<223> signal peptide
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<221> SITE
<222> (21) ... (43)
<223> framework 1
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<222> (44) ... (59)
<223> CDR1
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<221> SITE
<222> (60)...(74)
<223> framework 2
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<221> SITE
<222> (75) ... (81)
<223> CDR2
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<221> SITE
<222> (82)...(113)
<223> framework 3
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<221> SITE
<222> (114) ... (122)
<223> CDR3
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<221> SITE
<222> (123)...(132)
<223> framework 4
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<400> 2
Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
 1          5          10          15
Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
          20          25          30
Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
          35          40          45
Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys
          50          55          60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
65          70          75          80

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Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
 100 105 110
 Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 115 120 125
 Leu Glu Ile Lys
 130

<210> 3
 <211> 420
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(420)

<400> 3
 atg gga tgg agc tgt atc atc ctc ttc ttg gta tca aca gct aca agt 48
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15
 gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag 96
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 cct ggg act tca gtg aag ctg tcc tgc aag ggt tat ggc tac acc ttc 144
 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
 35 40 45
 acc agc tac tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt 192
 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60
 gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat 240
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80
 caa aaa ttc aag ggc aag gcc aca ttg act gta gac att tcc tcc agc 288
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
 85 90 95
 aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc 336
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac 384
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125
 tac tgg ggt caa ggc acc tca gtc acc gtc tcc tca 420
 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

<210> 4
 <211> 140

<212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)
 <223> signal peptide

<221> SITE
 <222> (20)...(49)
 <223> framework 1

<221> SITE
 <222> (50)...(54)
 <223> CDR1

<221> SITE
 <222> (55)...(68)
 <223> framework 2

<221> SITE
 <222> (69)...(85)
 <223> CDR2

<221> SITE
 <222> (86)...(117)
 <223> framework 3

<221> SITE
 <222> (118)...(129)
 <223> CDR3

<221> SITE
 <222> (130)...(140)
 <223> framework 4

<400> 4
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30
 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

<210> 5
 <211> 540

<212> DNA

<213> Artificial Sequence

<220>

<223> Portion of the heavy chain of LDP-02 with a heavy chain signal peptide

<221> CDS

<222> (1)...(540)

<400> 5

atg aaa tgc acc tgg gtc att ctc ttc ttg gta tca aca gct aca agt	48
Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser	
1 5 10 15	
gtc cac tcc cag gtc caa cta gtg cag tct ggg gct gag gtt aag aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggg gct tca gtg aag gtg tcc tgc aag ggt tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe	
35 40 45	
acc agc tac tgg atg cat tgg gtg agg cag gcg cct ggc caa cgt cta	192
Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu	
50 55 60	
gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat	240
Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn	
65 70 75 80	
caa aaa ttc aag gga cgc gtc aca ttg act gta gac att tcc gct agc	288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser	
85 90 95	
aca gcc tac atg gag ctc agc agc ctg aga tct gag gac act gcg gtc	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
100 105 110	
tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac	384
Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp	
115 120 125	
tac tgg ggt caa ggc acc ctg gtc acc gtc tcc tca gcc tcc acc aag	432
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys	
130 135 140	
ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg	480
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	
145 150 155 160	
ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg	528
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	
165 170 175	
gtg acg gtg tcg	540
Val Thr Val Ser	
180	

<210> 6
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Portion of the heavy chain of LDP-02 with a heavy chain signal peptide

<221> SITE
 <222> (19)...(20)
 <223> signal peptide cleavage site

<400> 6
 Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
 1 5 10 15
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
 50 55 60
 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
 115 120 125
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser
 180

<210> 7
 <211> 413
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Portion of the light chain LDP-02 with a light chain signal peptide

<221> CDS
 <222> (1)...(413)

<400> 7
 atgaagttgc ctgtaggct gttggtgctt ctgttgttct ggattcctgt ttccggaggt 60
 gatgttgta tgactcaaag tccactctcc ctgcctgtca cccctggaga accagcttct 120
 atctcttgca ggtctagtca gagtcttgca aagagttatg ggaacaccta tttgtcttgg 180
 tacctgcaga agcctggcca gtctccacag ctcctcatct atgggatttc caacagattt 240
 tctggggtgc cagacaggtt cagtggcagt gggttcaggga cagatttcac actcaagatc 300
 tcgcgagtag aggctgagga cgtgggagtg tattactgct tacaaggtac acatcagccc 360

tacacgttcg gacaggggac caaggtggaa ataaaacggg ctgatgcggc gcc

413

<210> 8

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Portion of the light chain of LDP-02 with a light chain signal peptide

<221> SITE

<222> (20)...(21)

<223> signal peptide cleavage site

<400> 8

Met	Lys	Leu	Pro	Val	Arg	Leu	Leu	Val	Leu	Leu	Phe	Trp	Ile	Pro	
1				5					10				15		
Val	Ser	Gly	Gly	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro
		20						25				30			
Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser
		35				40					45				
Leu	Ala	Lys	Ser	Tyr	Gly	Asn	Thr	Tyr	Leu	Ser	Trp	Tyr	Leu	Gln	Lys
	50				55				60						
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gly	Ile	Ser	Asn	Arg	Phe
65				70					75				80		
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe
			85					90					95		
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
		100				105						110			
Cys	Leu	Gln	Gly	Thr	His	Gln	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
	115					120						125			
Val	Glu	Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro						
	130					135									

<210> 9

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)...(16)

<223> CDR1 of the light chain of antibodies Act-1 and LDP-02

<400> 9

Arg	Ser	Ser	Gln	Ser	Leu	Ala	Lys	Ser	Tyr	Gly	Asn	Thr	Tyr	Leu	Ser
1				5					10					15	

<210> 10

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)...(7)
 <223> CDR2 of the light chain of antibodies Act-1 and
 LDP-02

<400> 10
 Gly Ile Ser Asn Arg Phe Ser
 1 5

<210> 11
 <211> 9
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(9)
 <223> CDR3 of the light chain of antibodies Act-1 and
 LDP-02

<400> 11
 Leu Gln Gly Thr His Gln Pro Tyr Thr
 1 5

<210> 12
 <211> 5
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(5)
 <223> CDR1 of the heavy chain of antibodies Act-1 and
 LDP-02

<400> 12
 Ser Tyr Trp Met His
 1 5

<210> 13
 <211> 17
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(17)
 <223> CDR2 of the heavy chain of antibodies Act-1 and
 LDP-02

<400> 13
 Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn Gln Lys Phe Lys
 1 5 10 15
 Gly

<210> 14
 <211> 12
 <212> PRT
 <213> Mus musculus

<220>
 <221> SITE
 <222> (1)...(12)
 <223> CDR3 of the heavy chain of antibodies Act-1 and
 LDP-02

<400> 14
 Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp Tyr
 1 5 10

<210> 15
 <211> 396
 <212> DNA
 <213> Mus musculus

<400> 15
 ttttatttcc agcttggtcc cccctccgaa cgtgtacggc tgatgtgtac cttgtaagca 60
 gtaatacatt cccaagtcct caggctttat tgtgctgata ttgagtgtga aatctgtccc 120
 tgaaccactg ccaactgaacc tgtctggcac ccagaaaaat ctgttggaat tcccatagat 180
 gaggagctgt ggagactggc caggcttgtg caggtagcaa gacaaatagg tgttccata 240
 actctttgca agactctgac tagacctgca agagatagaa acttgatctc caaagctgac 300
 aggcagggag agtggagttt gagtcaccac aacatcacct ccggaaacag gaatccagaa 360
 caacagaagc accaacagcc taacaggcaa cttcat 396

<210> 16
 <211> 420
 <212> DNA
 <213> Mus musculus

<400> 16
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 gtaacccctt cttgcacaat agtagaccgc agagtcctca gatgtcaggc tgctgagctg 120
 catgtaggct gtgctggagg aaatgtctac agtcaatgtg gccttgccct tgaatttttg 180
 attgtagtta gtattactct cagaaggatc aatctctccg atccactcaa ggccttgtcc 240
 aggcctctgc ttcacccagt gcatccagta gctgggtgaag gtgtagccat aacccttgca 300
 ggacagcttc actgaagtcc caggcttcac aagctcagcc ccaggctgct gcagttggac 360
 ctgggagtggt acacttgtag ctgttgatac caagaagagg atgatacagc tccatcccat 420